

RAW SEQUENCE LISTING

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Application Serial Number: 10/511,468A
Source: PC
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/511,468A

DATE: 04/14/2006
TIME: 11:16:57

Input Set : A:\2005-11-21 4614-0159PUS1.ST25.txt
Output Set: N:\CRF4\04142006\J511468A.raw

5 <110> APPLICANT: Soren Weis DAHL et al.
 7 <120> TITLE OF INVENTION: TRANSLOCATION DEPENDENT COMPLEMENTATION FOR DRUG SCREENING
 9 <130> FILE REFERENCE: 4614-0159PUS1
 11 <140> CURRENT APPLICATION NUMBER: US 10/511,468A
 12 <141> CURRENT FILING DATE: 2004-10-18
 14 <160> NUMBER OF SEQ ID NOS: 99
 16 <170> SOFTWARE: PatentIn version 3.1
 18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 238
 20 <212> TYPE: PRT
 21 <213> ORGANISM: Aequorea victoria
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 30 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 31 35 40 45
 33 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 34 50 55 60
 36 Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
 37 65 70 75 80
 39 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 40 85 90 95
 42 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 43 100 105 110
 45 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 46 115 120 125
 48 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 49 130 135 140
 51 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 52 145 150 155 160
 54 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
 55 165 170 175
 57 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
 58 180 185 190
 60 Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
 61 195 200 205
 63 Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
 64 210 215 220
 66 Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
 67 225 230 235
 69 <210> SEQ ID NO: 2

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70 <211> LENGTH: 238
 71 <212> TYPE: PRT
 72 <213> ORGANISM: Aequorea victoria
 74 <400> SEQUENCE: 2

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 78 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 79 20 25 30
 81 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 82 35 40 45
 84 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 85 50 55 60
 87 Ser Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
 88 65 70 75 80
 90 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 91 85 90 95
 93 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 94 100 105 110
 96 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 97 115 120 125
 99 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 100 130 135 140
 102 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 103 145 150 155 160
 105 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
 106 165 170 175
 108 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
 109 180 185 190
 111 Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
 112 195 200 205
 114 Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
 115 210 215 220
 117 Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
 118 225 230 235
 120 <210> SEQ ID NO: 3
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 123 <213> ORGANISM: Aequorea victoria
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 129 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 130 20 25 30
 132 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 133 35 40 45
 135 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 136 50 55 60
 138 Ser His Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
 139 65 70 75 80

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141 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 142 85 90 95
 144 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 145 100 105 110
 147 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 148 115 120 125
 150 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 151 130 135 140
 153 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 154 145 150 155 160
 156 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
 157 165 170 175
 159 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
 160 180 185 190
 162 Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
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 180 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 181 20 25 30
 183 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 184 35 40 45
 186 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 187 50 55 60
 189 Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 190 65 70 75 80
 192 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 193 85 90 95
 195 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 196 100 105 110
 198 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 199 115 120 125
 201 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 202 130 135 140
 204 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 205 145 150 155 160
 207 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 208 165 170 175
 210 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 211 180 185 190

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213 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 214 195 200 205
 216 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 217 210 215 220
 219 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 220 225 230 235
 222 <210> SEQ ID NO: 5
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 231 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 232 20 25 30
 234 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 235 35 40 45
 237 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 238 50 55 60
 240 Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 241 65 70 75 80
 243 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 244 85 90 95
 246 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 247 100 105 110
 249 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 250 115 120 125
 252 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 253 130 135 140
 255 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 256 145 150 155 160
 258 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 259 165 170 175
 261 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 262 180 185 190
 264 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu
 265 195 200 205
 267 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
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 271 225 230 235
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 275 <212> TYPE: PRT
 276 <213> ORGANISM: Aequorea victoria
 278 <400> SEQUENCE: 6
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 282 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly

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283 20 25 30
 285 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 286 35 40 45
 288 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 289 50 55 60
 291 Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 292 65 70 75 80
 294 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 295 85 90 95
 297 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 298 100 105 110
 301 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 302 115 120 125
 304 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 305 130 135 140
 307 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 308 145 150 155 160
 310 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 311 165 170 175
 313 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 314 180 185 190
 316 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu
 317 195 200 205
 319 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
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 332 <221> NAME/KEY: CDS
 333 <222> LOCATION: (3)..(116)
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 338 1 5 10 15
 340 gcc aac aag aag gag ctg gcc cag ctg aag tgg gag ctg cag gcc ctg 95
 341 Ala Asn Lys Lys Glu Leu Ala Gln Leu Lys Trp Glu Leu Gln Ala Leu
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 351 <213> ORGANISM: Homo sapiens
 353 <400> SEQUENCE: 8

VERIFICATION SUMMARY

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Input Set : A:\2005-11-21 4614-0159PUS1.ST25.txt

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